

WEST Search History

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DATE: Wednesday, August 16, 2006

| Hide? | <u>Set Name</u> | <u>Query</u> | <u>Hit Count</u> |
|--------------------------|--|---|----------------------|
| | <i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i> | | |
| <input type="checkbox"/> | L8 | L7 not l6 | 55 |
| <input type="checkbox"/> | L7 | L3 and kidney | 189 |
| <input type="checkbox"/> | L6 | l2 and (autoimmune or lupus or sle) | 152 |
| <input type="checkbox"/> | L5 | L4 and l1 | 1 |
| <input type="checkbox"/> | L4 | L2 same (autoimmune or lupus or sle) | 1 |
| <input type="checkbox"/> | L3 | l2 and (array or microarray or profile) | 227 |
| <input type="checkbox"/> | L2 | L1 same (expression or mRNA) | 308 |
| <input type="checkbox"/> | L1 | SFRP1 or FRP or SARP2 or (secreted adj (apoptosis or frizzled) adj related adj protein) | 18257 |

END OF SEARCH HISTORY

SYSTEM:OS - DIALOG OneSearch

- File 5:Biosis Previews(R) 1969-2006/Aug W1
(c) 2006 The Thomson Corporation
- File 6:NTIS 1964-2006/Aug W1
(c) 2006 NTIS, Intl Cpyrght All Rights Res
- File 8:Ei Compendex(R) 1970-2006/Aug W1
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(c) 2006 CSA.
- File 34:SciSearch(R) Cited Ref Sci 1990-2006/Aug W1
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- File 71:ELSEVIER BIOBASE 1994-2006/Aug W2
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- File 99:Wilson Appl. Sci & Tech Abs 1983-2006/Jul
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- File 135:NewsRx Weekly Reports 1995-2006/Aug W1
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- File 136:BioEngineering Abstracts 1966-2006/Jul
(c) 2006 CSA.
- File 143:Biol. & Agric. Index 1983-2006/Jul
(c) 2006 The HW Wilson Co
- File 144:Pascal 1973-2006/Jul W4
(c) 2006 INIST/CNRS
- File 155:MEDLINE(R) 1950-2006/Aug 15
(c) format only 2006 Dialog
- File 172:EMBASE Alert 2006/Aug 16
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- File 266:FEDRIP 2005/Dec
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- File 315:ChemEng & Biotec Abs 1970-2006/Jul
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- File 357:Derwent Biotech Res. _1982-2006/Aug W2
(c) 2006 The Thomson Corp.
- File 358:Current BioTech Abs 1983-2006/Jan
(c) 2006 DECHEMA
- File 369:New Scientist 1994-2006/Jul W3
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- File 370:Science 1996-1999/Jul W3
(c) 1999 AAAS
- *File 370: This file is closed (no updates). Use File 47 for more current information.
- File 399:CA SEARCH(R) 1967-2006/UD=14508
(c) 2006 American Chemical Society
- *File 399: Use is subject to the terms of your user/customer agreement.
IPCR/8 classification codes now searchable as IC=. See HELP NEWSIPCR.

Set Items Description .

--- -----

? s SFRP1 or (secreted (w) frizzle\$ (w) related (w) protein) or SARP2 or SFRP-1

555 SFRP1

328608 SECRETED

0 FRIZZLE\$

7877444 RELATED

10289834 PROTEIN

0 SECRETED(W)FRIZZLE\$(W)RELATED(W)PROTEIN

41 SARP2

33 SFRP-1

S1 627 SFRP1 OR (SECRETED (W) FRIZZLE\$ (W) RELATED (W) PROTEIN)

OR SARP2 OR SFRP-1

? s SFRP1 or (secreted (w) frizzled (w) related (w) protein) or SARP2 or SFRP-1

Processing

Processed 20 of 26 files ...

Completed processing all files

555 SFRP1

328608 SECRETED

6916 FRIZZLED

7877444 RELATED

10289834 PROTEIN

1027 SECRETED(W)FRIZZLED(W)RELATED(W)PROTEIN

41 SARP2

33 SFRP-1

S2 1377 SFRP1 OR (SECRETED (W) FRIZZLED (W) RELATED (W) PROTEIN)

OR SARP2 OR SFRP-1

s s2 and (autoimmune or lupus or sle or RA or rheumatoid)

1377 S2

491380 AUTOIMMUNE

271377 LUPUS

78024 SLE

617272 RA

422382 RHEUMATOID

S3 42 S2 AND (AUTOIMMUNE OR LUPUS OR SLE OR RA OR RHEUMATOID)

? rd s3

S4 17 RD S3 (unique items)

? s s2 and (expression or mRNA or profile)

1377 S2

6020558 EXPRESSION

1391965 MRNA

1135906 PROFILE

S5 1015 S2 AND (EXPRESSION OR MRNA OR PROFILE)

? s s5 and (array or microarray)

1015 S5

584443 ARRAY

164260 MICROARRAY

S6 188 S5 AND (ARRAY OR MICROARRAY)

? rd s6

S7 84 RD S6 (unique items)

? s s7 not s3

84 S7

42 S3

S8 80 S7 NOT S3t s10/6/1-38

```

Run on:      August  3, 2006, 10:58:55 ; Search time 24395 Seconds
              (without alignments)
              11714.738 Million cell updates/sec

Title:       US-10-786-720-15
Perfect score: 4469
Sequence:    1 cctgcagcctccggagtcag.....taatcaatgaaaaaaaaaaaa 4469

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:    6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 150 summaries
    
```

```

Database :      GenEmbl:*
                1:  gb_env:*
                2:  gb_pat:*
                3:  gb_ph:*
                4:  gb_pl:*
                5:  gb_pr:*
                6:  gb_ro:*
                7:  gb_sts:*
                8:  gb_sy:*
                9:  gb_un:*
               10:  gb_vi:*
               11:  gb_ov:*
               12:  gb_htg:*
               13:  gb_in:*
               14:  gb_om:*
               15:  gb_ba:*
    
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | | | |
|-----------|---------|-------|--------------|----|----------|--------------------|
| Result | % Query | | | | | |
| | No. | Score | Match Length | DB | ID | Description |
| 1 | 4469 | 100.0 | 4469 | 2 | CS025753 | CS025753 Sequence |
| 2 | 4469 | 100.0 | 4469 | 2 | AX236302 | AX236302 Sequence |
| 3 | 4469 | 100.0 | 4469 | 2 | AX578081 | AX578081 Sequence |
| 4 | 4469 | 100.0 | 4469 | 5 | AF056087 | AF056087 Homo sapi |
| 5 | 4356.8 | 97.5 | 4500 | 2 | AR253209 | AR253209 Sequence |
| 6 | 4339.4 | 97.1 | 4482 | 5 | BC036503 | BC036503 Homo sapi |
| 7 | 3935 | 88.1 | 4245 | 2 | AR129158 | AR129158 Sequence |
| 8 | 3580.6 | 80.1 | 3670 | 2 | BD135188 | BD135188 Human nuc |
| 9 | 3580.6 | 80.1 | 3670 | 2 | AX017498 | AX017498 Sequence |
| 10 | 3504.8 | 78.4 | 3872 | 2 | CQ850220 | CQ850220 Sequence |
| 11 | 3504.8 | 78.4 | 3872 | 5 | AK127331 | AK127331 Homo sapi |
| 12 | 3448 | 77.2 | 171133 | 5 | AC103846 | AC103846 Homo sapi |
| 13 | 3448 | 77.2 | 188270 | 5 | AC104393 | AC104393 Homo sapi |

| | | | | | | |
|------|--------|------|--------|----|-----------|--------------------|
| 14 | 3081 | 68.9 | 3181 | 2 | BD205077 | BD205077 Human nuc |
| 15 | 3081 | 68.9 | 3181 | 2 | AX013686 | AX013686 Sequence |
| 16 | 2465.4 | 55.2 | 2602 | 2 | AX099741 | AX099741 Sequence |
| 17 | 2075 | 46.4 | 2075 | 2 | AR253206 | AR253206 Sequence |
| 18 | 2075 | 46.4 | 2075 | 2 | AR361924 | AR361924 Sequence |
| 19 | 2075 | 46.4 | 2075 | 2 | AR433000 | AR433000 Sequence |
| 20 | 2075 | 46.4 | 2075 | 2 | AX482567 | AX482567 Sequence |
| 21 | 2075 | 46.4 | 2075 | 2 | AX565707 | AX565707 Sequence |
| 22 | 2075 | 46.4 | 2075 | 2 | AX597107 | AX597107 Sequence |
| 23 | 2075 | 46.4 | 2075 | 2 | AX701365 | AX701365 Sequence |
| 24 | 2075 | 46.4 | 2075 | 5 | AF001900 | AF001900 Homo sapi |
| 25 | 2062 | 46.1 | 2078 | 2 | AR253205 | AR253205 Sequence |
| 26 | 1991.6 | 44.6 | 2094 | 5 | AF017987 | AF017987 Homo sapi |
| 27 | 1476.6 | 33.0 | 4240 | 14 | BTU85945 | U85945 Bos taurus |
| 28 | 1256.6 | 28.1 | 1308 | 2 | BD217906 | BD217906 Gene fami |
| 29 | 1196.8 | 26.8 | 4375 | 6 | BC094662 | BC094662 Mus muscu |
| 30 | 923.8 | 20.7 | 945 | 8 | AY891055 | AY891055 Synthetic |
| 31 | 923.8 | 20.7 | 945 | 8 | BT019677 | BT019677 Synthetic |
| c 32 | 906.4 | 20.3 | 197427 | 12 | AC182062 | AC182062 Bos tauru |
| 33 | 899.8 | 20.1 | 942 | 2 | AR361925 | AR361925 Sequence |
| 34 | 899.8 | 20.1 | 942 | 2 | AX482568 | AX482568 Sequence |
| 35 | 896.8 | 20.1 | 1017 | 2 | AR361926 | AR361926 Sequence |
| 36 | 896.2 | 20.1 | 1340 | 6 | BC024495 | BC024495 Mus muscu |
| 37 | 886.4 | 19.8 | 2659 | 6 | MMU88566 | U88566 Mus musculu |
| 38 | 828.2 | 18.5 | 155691 | 5 | AC016868 | AC016868 Homo sapi |
| 39 | 776.2 | 17.4 | 2124 | 2 | AR253208 | AR253208 Sequence |
| 40 | 703.6 | 15.7 | 3065 | 11 | GGA404652 | AJ404652 Gallus ga |
| 41 | 684.2 | 15.3 | 804 | 2 | AR361929 | AR361929 Sequence |
| 42 | 621.2 | 13.9 | 741 | 2 | AR361928 | AR361928 Sequence |
| 43 | 609.6 | 13.6 | 1146 | 2 | AX565729 | AX565729 Sequence |
| 44 | 609.6 | 13.6 | 1146 | 2 | AX597129 | AX597129 Sequence |
| 45 | 609.6 | 13.6 | 1146 | 2 | AX701375 | AX701375 Sequence |
| 46 | 609.4 | 13.6 | 770 | 5 | HSA325301 | AJ325301 Homo sapi |
| 47 | 609 | 13.6 | 726 | 7 | BV208829 | BV208829 SFRP1_189 |
| c 48 | 588 | 13.2 | 241809 | 6 | AC139848 | AC139848 Mus muscu |
| c 49 | 536 | 12.0 | 184377 | 6 | AC147247 | AC147247 Mus muscu |
| c 50 | 527 | 11.8 | 548 | 2 | AR280573 | AR280573 Sequence |

Run on: August 3, 2006, 10:56:23 ; Search time 2549 Seconds
 (without alignments)
 12224.001 Million cell updates/sec

Title: US-10-786-720-15
 Perfect score: 4469
 Sequence: 1 cctgcagcctccggagtcag.....taatcaatgaaaaaaaaaaaa 4469

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : N_Geneseq_8:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| % Query | | | | | | |
|---------|--------|-------|--------|----|----------|--------------------|
| Result | Score | Match | Length | DB | ID | Description |
| No. | | | | | | |
| ----- | | | | | | |
| 1 | 4469 | 100.0 | 4469 | 4 | AAS12954 | Aas12954 Human Fri |
| 2 | 4469 | 100.0 | 4469 | 6 | ABT10165 | Abt10165 Human bre |
| 3 | 4469 | 100.0 | 4469 | 8 | ABZ34845 | Abz34845 Coding se |
| 4 | 4469 | 100.0 | 4469 | 12 | ADP21417 | Adp21417 Gene SFRP |
| 5 | 4469 | 100.0 | 4469 | 13 | ADR24996 | Adr24996 Breast ca |
| 6 | 4469 | 100.0 | 4469 | 13 | ADR99015 | Adr99015 Secreted |
| 7 | 4469 | 100.0 | 4469 | 13 | AEA64538 | Aea64538 Human lup |
| 8 | 4469 | 100.0 | 4469 | 14 | ADV44809 | Adv44809 Secreted |
| 9 | 4469 | 100.0 | 4469 | 14 | ADX58915 | Adx58915 Human reg |
| c 10 | 4439.8 | 99.3 | 4608 | 14 | AED73309 | Aed73309 Human pla |
| 11 | 4393.4 | 98.3 | 4462 | 8 | ABX77526 | Abx77526 Different |
| 12 | 4355.4 | 97.5 | 4616 | 4 | AAH72901 | Aah72901 Human cer |
| 13 | 4355.2 | 97.5 | 4497 | 2 | AAV84395 | Aav84395 Human Fri |

| | | | | | | | |
|---|----|--------|------|------|----|----------|--------------------|
| | 14 | 4335.4 | 97.0 | 4451 | 8 | ABZ82226 | Abz82226 Human sFR |
| | 15 | 3935 | 88.1 | 4245 | 4 | AAF80506 | Aaf80506 Cell prol |
| | 16 | 3580.6 | 80.1 | 3670 | 2 | AAZ33577 | Aaz33577 Human bre |
| | 17 | 3504.8 | 78.4 | 3872 | 13 | ADR07183 | Adr07183 Full leng |
| | 18 | 3102.6 | 69.4 | 3215 | 3 | AAC77657 | Aac77657 Human can |
| | 19 | 3090.4 | 69.2 | 3216 | 2 | AAZ33608 | Aaz33608 Human bre |
| | 20 | 3069 | 68.7 | 3180 | 2 | AAZ42127 | Aaz42127 Human nor |
| | 21 | 2465.4 | 55.2 | 2602 | 12 | ADP68535 | Adp68535 Human sec |
| | 22 | 2075 | 46.4 | 2075 | 4 | AAD17401 | Aad17401 Human sec |
| | 23 | 2075 | 46.4 | 2075 | 6 | ABV73022 | Abv73022 Human sec |
| | 24 | 2075 | 46.4 | 2075 | 8 | ABX75330 | Abx75330 Human cDN |
| | 25 | 2075 | 46.4 | 2075 | 8 | AAD52558 | Aad52558 FRP DNA. |
| | 26 | 2075 | 46.4 | 2075 | 12 | ADH43319 | Adh43319 Human sec |
| | 27 | 2074.6 | 46.4 | 2075 | 10 | ADC71197 | Adc71197 Human sec |
| | 28 | 2059 | 46.1 | 2072 | 8 | ABZ81830 | Abz81830 Receptor |
| | 29 | 1991.6 | 44.6 | 2094 | 8 | ABZ82228 | Abz82228 Human sec |
| | 30 | 1256.6 | 28.1 | 1308 | 2 | AAV19115 | Aav19115 Human sec |
| c | 31 | 978.6 | 21.9 | 1247 | 13 | ACN41451 | Acn41451 Human dia |
| | 32 | 942 | 21.1 | 942 | 8 | ABZ82227 | Abz82227 Human sec |
| | 33 | 942 | 21.1 | 942 | 9 | ACC81035 | Acc81035 Human emb |
| | 34 | 899.8 | 20.1 | 942 | 6 | ABV73023 | Abv73023 Human sec |
| | 35 | 899.8 | 20.1 | 942 | 10 | ADC71198 | Adc71198 ORF of th |
| | 36 | 899.8 | 20.1 | 942 | 12 | ADH43320 | Adh43320 Human sec |
| | 37 | 896.8 | 20.1 | 1017 | 10 | ADC71192 | Adc71192 DNA encod |
| | 38 | 896.8 | 20.1 | 1017 | 12 | ADH43314 | Adh43314 Human sFR |
| | 39 | 812.2 | 18.2 | 945 | 9 | ACC81034 | Acc81034 Murine em |
| | 40 | 800.8 | 17.9 | 2124 | 2 | AAV84394 | Aav84394 Partial F |
| | 41 | 684.2 | 15.3 | 804 | 10 | ADC71195 | Adc71195 DNA encod |
| | 42 | 684.2 | 15.3 | 804 | 12 | ADH43317 | Adh43317 Human sec |
| | 43 | 621.2 | 13.9 | 741 | 10 | ADC71194 | Adc71194 DNA encod |
| | 44 | 621.2 | 13.9 | 741 | 12 | ADH43316 | Adh43316 Human sec |
| | 45 | 609.6 | 13.6 | 1146 | 8 | ABX75340 | Abx75340 Human cDN |
| | 46 | 609.6 | 13.6 | 1146 | 8 | AAD52570 | Aad52570 SRFP 1 DN |
| | 47 | 609.6 | 13.6 | 1146 | 8 | ABZ81842 | Abz81842 WIF-1 nuc |
| | 48 | 551.8 | 12.3 | 566 | 14 | ACL62743 | Acl62743 Human col |
| c | 49 | 527 | 11.8 | 548 | 4 | AAF17593 | Aaf17593 Human bre |
| c | 50 | 527 | 11.8 | 548 | 4 | AAS47023 | Aas47023 Human bre |

Run on: August 3, 2006, 11:01:00 ; Search time 765 Seconds
 (without alignments)
 10930.700 Million cell updates/sec

Title: US-10-786-720-15
 Perfect score: 4469
 Sequence: 1 cctgcagcctccggagtcag.....taatcaatgaaaaaaaaaaaa 4469

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : Issued Patents_NA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|--------|---------|--------------|-------|---------------------------------------|
| 1 | 4469 | 100.0 | 4469 | 3 | US-09-949-016-428 Sequence 428, App |
| 2 | 4469 | 100.0 | 4469 | 5 | US-09-796-008-1 Sequence 1, Appli |
| 3 | 4356.8 | 97.5 | 4500 | 3 | US-09-087-031E-27 Sequence 27, Appl |
| 4 | 3935 | 88.1 | 4245 | 3 | US-09-276-531-16 Sequence 16, Appl |
| 5 | 3258.8 | 72.9 | 7360 | 3 | US-09-949-016-15054 Sequence 15054, A |
| 6 | 3258.4 | 72.9 | 3360 | 3 | US-09-949-016-3312 Sequence 3312, Ap |
| 7 | 2075 | 46.4 | 2075 | 3 | US-09-087-031E-2 Sequence 2, Appli |
| 8 | 2075 | 46.4 | 2075 | 3 | US-09-546-043-1 Sequence 1, Appli |
| 9 | 2075 | 46.4 | 2075 | 3 | US-09-514-885-2 Sequence 2, Appli |
| 10 | 2062 | 46.1 | 2078 | 3 | US-09-087-031E-1 Sequence 1, Appli |
| 11 | 1256.6 | 28.1 | 1308 | 3 | US-08-937-067-18 Sequence 18, Appl |
| 12 | 899.8 | 20.1 | 942 | 3 | US-09-546-043-2 Sequence 2, Appli |
| 13 | 896.8 | 20.1 | 1017 | 3 | US-09-546-043-9 Sequence 9, Appli |
| 14 | 776.2 | 17.4 | 2124 | 3 | US-09-087-031E-26 Sequence 26, Appl |
| 15 | 684.2 | 15.3 | 804 | 3 | US-09-546-043-12 Sequence 12, Appl |
| 16 | 621.2 | 13.9 | 741 | 3 | US-09-546-043-11 Sequence 11, Appl |
| c 17 | 600.6 | 13.4 | 601 | 3 | US-09-949-016-26352 Sequence 26352, A |
| c 18 | 600.6 | 13.4 | 601 | 3 | US-09-949-016-119368 Sequence 119368, |

| | | | | | | | |
|---|----|-------|------|-------|---|----------------------|-------------------|
| c | 19 | 597.4 | 13.4 | 601 | 3 | US-09-949-016-26353 | Sequence 26353, A |
| c | 20 | 597.4 | 13.4 | 601 | 3 | US-09-949-016-119369 | Sequence 119369, |
| c | 21 | 587 | 13.1 | 601 | 3 | US-09-949-016-26354 | Sequence 26354, A |
| c | 22 | 587 | 13.1 | 601 | 3 | US-09-949-016-119370 | Sequence 119370, |
| c | 23 | 579.6 | 13.0 | 601 | 3 | US-09-949-016-26355 | Sequence 26355, A |
| c | 24 | 579.6 | 13.0 | 601 | 3 | US-09-949-016-119371 | Sequence 119371, |
| c | 25 | 527 | 11.8 | 548 | 3 | US-09-222-575-78 | Sequence 78, Appl |
| c | 26 | 527 | 11.8 | 548 | 3 | US-09-389-681-78 | Sequence 78, Appl |
| c | 27 | 527 | 11.8 | 548 | 3 | US-09-620-405B-78 | Sequence 78, Appl |
| c | 28 | 527 | 11.8 | 548 | 3 | US-09-339-338-78 | Sequence 78, Appl |
| c | 29 | 527 | 11.8 | 548 | 3 | US-09-433-826B-78 | Sequence 78, Appl |
| c | 30 | 527 | 11.8 | 548 | 3 | US-09-604-287A-78 | Sequence 78, Appl |
| c | 31 | 527 | 11.8 | 548 | 3 | US-09-285-480-78 | Sequence 78, Appl |
| c | 32 | 527 | 11.8 | 548 | 3 | US-09-834-759-78 | Sequence 78, Appl |
| c | 33 | 527 | 11.8 | 548 | 3 | US-09-590-751A-78 | Sequence 78, Appl |
| c | 34 | 527 | 11.8 | 548 | 3 | US-09-551-621-78 | Sequence 78, Appl |
| c | 35 | 527 | 11.8 | 548 | 3 | US-09-551-621A-78 | Sequence 78, Appl |
| c | 36 | 527 | 11.8 | 548 | 3 | US-10-076-622-78 | Sequence 78, Appl |
| c | 37 | 527 | 11.8 | 548 | 4 | US-10-124-805-78 | Sequence 78, Appl |
| | 38 | 468.8 | 10.5 | 588 | 3 | US-09-546-043-10 | Sequence 10, Appl |
| | 39 | 444 | 9.9 | 690 | 3 | US-09-546-043-13 | Sequence 13, Appl |
| | 40 | 400 | 9.0 | 1984 | 3 | US-08-937-067-5 | Sequence 5, Appli |
| | 41 | 399.2 | 8.9 | 1905 | 3 | US-09-949-016-429 | Sequence 429, App |
| | 42 | 393.4 | 8.8 | 1719 | 3 | US-09-949-016-1835 | Sequence 1835, Ap |
| c | 43 | 320 | 7.2 | 601 | 3 | US-09-949-016-26356 | Sequence 26356, A |
| c | 44 | 320 | 7.2 | 601 | 3 | US-09-949-016-119372 | Sequence 119372, |
| | 45 | 253.2 | 5.7 | 9086 | 3 | US-09-949-016-13577 | Sequence 13577, A |
| | 46 | 253.2 | 5.7 | 85369 | 3 | US-09-949-016-12171 | Sequence 12171, A |
| | 47 | 238.4 | 5.3 | 240 | 5 | US-09-796-008-3 | Sequence 3, Appli |
| | 48 | 233.6 | 5.2 | 2030 | 3 | US-08-937-067-1 | Sequence 1, Appli |
| | 49 | 224.8 | 5.0 | 2027 | 5 | US-08-949-904A-1 | Sequence 1, Appli |
| | 50 | 223.4 | 5.0 | 1869 | 3 | US-09-148-545-56 | Sequence 56, Appl |

Run on: August 3, 2006, 11:09:19 ; Search time 4965 Seconds
 (without alignments)
 11060.109 Million cell updates/sec

Title: US-10-786-720-15
 Perfect score: 4469
 Sequence: 1 cctgcagcctccggagtcag.....taatcaatgaaaaaaaaaaaa 4469

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | Length | DB | ID | Description |
|------------|--------|---------|--|--------|----|-------------------|-------------------|
| | | Match | | | | | |
| 1 | 4469 | 100.0 | | 4469 | 3 | US-09-796-008-1 | Sequence 1, Appli |
| 2 | 4469 | 100.0 | | 4469 | 7 | US-10-133-937-42 | Sequence 42, Appl |
| 3 | 4469 | 100.0 | | 4469 | 7 | US-10-172-118-857 | Sequence 857, App |
| 4 | 4469 | 100.0 | | 4469 | 7 | US-10-159-563-42 | Sequence 42, Appl |
| 5 | 4469 | 100.0 | | 4469 | 8 | US-10-342-887-857 | Sequence 857, App |
| 6 | 4469 | 100.0 | | 4469 | 9 | US-10-786-720-15 | Sequence 15, Appl |
| 7 | 4469 | 100.0 | | 4469 | 9 | US-10-788-792-21 | Sequence 21, Appl |
| 8 | 4469 | 100.0 | | 4469 | 9 | US-10-473-974-203 | Sequence 203, App |
| 9 | 4469 | 100.0 | | 4469 | 9 | US-10-817-525-1 | Sequence 1, Appli |
| 10 | 4469 | 100.0 | | 4469 | 16 | US-11-245-147-203 | Sequence 203, App |
| c 11 | 4439.8 | 99.3 | | 4608 | 10 | US-10-821-234-137 | Sequence 137, App |
| 12 | 4393.4 | 98.3 | | 4462 | 3 | US-09-974-298-28 | Sequence 28, Appl |

| | | | | | | |
|------|--------|------|------|----|-----------------------|-------------------|
| 13 | 4356.8 | 97.5 | 4500 | 7 | US-10-138-434A-27 | Sequence 27, Appl |
| 14 | 3102.6 | 69.4 | 3215 | 3 | US-09-925-301-51 | Sequence 51, Appl |
| 15 | 2465.4 | 55.2 | 2602 | 8 | US-10-666-851-1 | Sequence 1, Appli |
| 16 | 2075 | 46.4 | 2075 | 7 | US-10-138-434A-2 | Sequence 2, Appli |
| 17 | 2075 | 46.4 | 2075 | 7 | US-10-425-586-1 | Sequence 1, Appli |
| 18 | 2075 | 46.4 | 2075 | 8 | US-10-466-136-1 | Sequence 1, Appli |
| 19 | 2062 | 46.1 | 2078 | 7 | US-10-138-434A-1 | Sequence 1, Appli |
| 20 | 1991.6 | 44.6 | 2094 | 10 | US-10-756-149-3306 | Sequence 3306, Ap |
| 21 | 1256.6 | 28.1 | 1308 | 6 | US-10-146-474-18 | Sequence 18, Appl |
| 22 | 1256.6 | 28.1 | 1308 | 8 | US-10-301-764-18 | Sequence 18, Appl |
| 23 | 899.8 | 20.1 | 942 | 7 | US-10-425-586-2 | Sequence 2, Appli |
| 24 | 899.8 | 20.1 | 942 | 8 | US-10-466-136-2 | Sequence 2, Appli |
| 25 | 896.8 | 20.1 | 1017 | 7 | US-10-425-586-9 | Sequence 9, Appli |
| 26 | 776.2 | 17.4 | 2124 | 7 | US-10-138-434A-26 | Sequence 26, Appl |
| 27 | 684.2 | 15.3 | 804 | 7 | US-10-425-586-12 | Sequence 12, Appl |
| 28 | 621.2 | 13.9 | 741 | 7 | US-10-425-586-11 | Sequence 11, Appl |
| 29 | 571.4 | 12.8 | 630 | 12 | US-10-301-480-560598 | Sequence 560598, |
| 30 | 571.4 | 12.8 | 630 | 12 | US-10-301-480-1174007 | Sequence 1174007, |
| c 31 | 527 | 11.8 | 548 | 3 | US-09-604-287A-78 | Sequence 78, Appl |
| c 32 | 527 | 11.8 | 548 | 3 | US-09-834-759-78 | Sequence 78, Appl |
| c 33 | 527 | 11.8 | 548 | 3 | US-09-339-338-78 | Sequence 78, Appl |
| c 34 | 527 | 11.8 | 548 | 3 | US-09-551-621-78 | Sequence 78, Appl |
| c 35 | 527 | 11.8 | 548 | 6 | US-10-007-805-78 | Sequence 78, Appl |
| c 36 | 527 | 11.8 | 548 | 6 | US-10-076-622-78 | Sequence 78, Appl |
| c 37 | 527 | 11.8 | 548 | 7 | US-10-124-805-78 | Sequence 78, Appl |
| c 38 | 527 | 11.8 | 548 | 7 | US-10-441-893-78 | Sequence 78, Appl |
| c 39 | 527 | 11.8 | 548 | 16 | US-11-226-869-78 | Sequence 78, Appl |
| 40 | 497 | 11.1 | 549 | 6 | US-10-027-632-93316 | Sequence 93316, A |
| 41 | 497 | 11.1 | 549 | 6 | US-10-027-632-305035 | Sequence 305035, |
| 42 | 497 | 11.1 | 549 | 7 | US-10-027-632-93316 | Sequence 93316, A |
| 43 | 497 | 11.1 | 549 | 7 | US-10-027-632-305035 | Sequence 305035, |
| c 44 | 482 | 10.8 | 501 | 3 | US-09-954-531-885 | Sequence 885, App |
| c 45 | 482 | 10.8 | 501 | 3 | US-09-954-531-1298 | Sequence 1298, Ap |
| c 46 | 482 | 10.8 | 501 | 10 | US-10-843-641A-1952 | Sequence 1952, Ap |
| c 47 | 482 | 10.8 | 501 | 10 | US-10-843-641A-2365 | Sequence 2365, Ap |
| 48 | 468.8 | 10.5 | 588 | 7 | US-10-425-586-10 | Sequence 10, Appl |
| 49 | 444 | 9.9 | 690 | 7 | US-10-425-586-13 | Sequence 13, Appl |
| 50 | 427.6 | 9.6 | 445 | 8 | US-10-242-535A-43352 | Sequence 43352, A |

Run on: August 3, 2006, 11:00:10 ; Search time 19407 Seconds
 (without alignments)
 12876.977 Million cell updates/sec

Title: US-10-786-720-15
 Perfect score: 4469
 Sequence: 1 cctgcagcctccggagtcag.....taatcaatgaaaaaaaaaaaa 4469

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | % | | | | | Description | |
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| | No. | Score | Query Match | Length | ID | | |
| c | 1 | 933.2 | 20.9 | 946 | 6 | BC004466 | BC004466 Homo sapi |
| | 2 | 898 | 20.1 | 919 | 6 | CR613872 | CR613872 full-leng |
| | 3 | 894.8 | 20.0 | 919 | 4 | BX343566 | BX343566 BX343566 |
| | 4 | 891 | 19.9 | 2704 | 6 | AK088868 | AK088868 Mus muscu |
| | 5 | 887.6 | 19.9 | 918 | 1 | AL528023 | AL528023 AL528023 |
| | 6 | 845.6 | 18.9 | 887 | 4 | BX402193 | BX402193 BX402193 |
| | 7 | 821.8 | 18.4 | 911 | 5 | CD519089 | CD519089 AGENCOURT |
| | 8 | 815.6 | 18.3 | 908 | 1 | AU125245 | AU125245 AU125245 |
| | 9 | 796.2 | 17.8 | 801 | 9 | CX781693 | CX781693 HESC3_8_B |
| | 10 | 782.6 | 17.5 | 838 | 2 | BG682306 | BG682306 602629621 |
| | 11 | 780.8 | 17.5 | 891 | 8 | CV810231 | CV810231 AGENCOURT |
| | 12 | 778.2 | 17.4 | 1011 | 3 | BU196604 | BU196604 AGENCOURT |
| | 13 | 768 | 17.2 | 837 | 1 | AU131621 | AU131621 AU131621 |
| | 14 | 760.4 | 17.0 | 763 | 9 | CX786676 | CX786676 HESC3 63 |

| | | | | | | | | |
|---|----|-------|------|------|---|----------|----------|-----------|
| | 15 | 759.8 | 17.0 | 785 | 9 | CX781701 | CX781701 | HESC3_8_C |
| | 16 | 754.2 | 16.9 | 2298 | 6 | AK081052 | AK081052 | Mus muscu |
| | 17 | 748.6 | 16.8 | 782 | 9 | DA571541 | DA571541 | DA571541 |
| c | 18 | 748.6 | 16.8 | 886 | 1 | AL528022 | AL528022 | AL528022 |
| | 19 | 746 | 16.7 | 952 | 8 | CO580514 | CO580514 | ILLUMIGEN |
| | 20 | 744.4 | 16.7 | 884 | 2 | BG681605 | BG681605 | 602628094 |
| | 21 | 736.8 | 16.5 | 764 | 1 | AU123839 | AU123839 | AU123839 |
| | 22 | 736.8 | 16.5 | 814 | 5 | CD644680 | CD644680 | AGENCOURT |
| | 23 | 732.8 | 16.4 | 913 | 3 | BQ879583 | BQ879583 | AGENCOURT |
| c | 24 | 727.8 | 16.3 | 803 | 5 | CD616079 | CD616079 | 56076764J |
| | 25 | 725.8 | 16.2 | 878 | 3 | BQ876624 | BQ876624 | AGENCOURT |
| | 26 | 721.4 | 16.1 | 762 | 8 | CN271890 | CN271890 | 170004245 |
| | 27 | 720.4 | 16.1 | 898 | 3 | BQ680787 | BQ680787 | AGENCOURT |
| | 28 | 718.6 | 16.1 | 864 | 5 | CD558546 | CD558546 | AGENCOURT |
| | 29 | 715.4 | 16.0 | 750 | 8 | CN271875 | CN271875 | 170005313 |
| | 30 | 711 | 15.9 | 922 | 3 | BQ932355 | BQ932355 | AGENCOURT |
| | 31 | 709.8 | 15.9 | 734 | 8 | CN271881 | CN271881 | 170006001 |
| | 32 | 709.4 | 15.9 | 723 | 4 | CA389569 | CA389569 | cs100d05. |
| | 33 | 708.6 | 15.9 | 762 | 1 | AU125808 | AU125808 | AU125808 |
| | 34 | 704.6 | 15.8 | 757 | 8 | CN271867 | CN271867 | 170005327 |
| c | 35 | 694.4 | 15.5 | 703 | 4 | CA413793 | CA413793 | UI-H-EZ0- |
| c | 36 | 693.8 | 15.5 | 701 | 4 | CA313964 | CA313964 | UI-CF-FN0 |
| c | 37 | 689.2 | 15.4 | 701 | 3 | BM670202 | BM670202 | UI-E-DW1- |
| | 38 | 681 | 15.2 | 823 | 1 | AU127052 | AU127052 | AU127052 |
| | 39 | 672.6 | 15.1 | 903 | 5 | CD244905 | CD244905 | AGENCOURT |
| | 40 | 667.4 | 14.9 | 792 | 2 | BG698901 | BG698901 | 602703318 |
| | 41 | 665 | 14.9 | 881 | 2 | BG253035 | BG253035 | 602365657 |
| | 42 | 664.8 | 14.9 | 779 | 4 | CB247875 | CB247875 | UI-M-FI0- |
| | 43 | 662.6 | 14.8 | 982 | 3 | BU501489 | BU501489 | AGENCOURT |
| | 44 | 661.8 | 14.8 | 741 | 8 | CR769220 | CR769220 | DKFZp469B |
| | 45 | 661.2 | 14.8 | 928 | 2 | BG120117 | BG120117 | 602353481 |
| | 46 | 660 | 14.8 | 779 | 5 | CD643855 | CD643855 | AGENCOURT |
| | 47 | 658.2 | 14.7 | 907 | 2 | BG119546 | BG119546 | 602347246 |
| c | 48 | 657.2 | 14.7 | 706 | 4 | CA434170 | CA434170 | UI-H-DH0- |
| | 49 | 655.4 | 14.7 | 738 | 3 | BQ771388 | BQ771388 | UI-M-FI0- |
| c | 50 | 654.4 | 14.6 | 660 | 3 | BM970588 | BM970588 | UI-CF-EC1 |